

25 Apr 2007

Alignment Results

EXHIBIT A

Alignment: Global Protein alignment against reference molecule
Parameters: Scoring matrix: BLOSUM 62

Reference molecule: SEQIDNO:2, Region 1-788

Number of sequences to align: 3

Settings: Similarity significance value cutoff: >= 60%



Summary of Percent Matches:

Reference:	SEQIDNO:2	1 -	788	(788 aa)	--
Sequence 2:	SEQIDNO:11	1 -	788	(788 aa)	97%
Sequence 3:	SEQIDNO:32	1 -	788	(788 aa)	99%

SEQIDNO:2	1	MNKNNTKLSTRALPSFIDYFNGIYGATGIKDIMNMIFKTDGGNLTLDEILKNQQLNE
SEQIDNO:11	1D.....D
SEQIDNO:32	1	..M.....NA.....
SEQIDNO:2	61	ISGLDGVNGSLNDLIAQGNLNTLSKEILKIANEQNQVLNDVNNKLD AINTMLHIYLPK
SEQIDNO:11	61RV.....
SEQIDNO:32	61
SEQIDNO:2	121	ITSMLSDVMKQNYALS LQIEYLSKQLQEISDKLDIINVNVLINSTLTEITPAYQRIKYVN
SEQIDNO:11	121
SEQIDNO:32	121
SEQIDNO:2	181	EKFEELTFATETTLKVKKDSSPADILDELTELAKSVTKNDVDGFEFYLNTHDVMVG
SEQIDNO:11	181SS.....G.....
SEQIDNO:32	181
SEQIDNO:2	241	NNLFGRSALKTASELIAKENVKTS GSEVGNVYNFLIVLTALQAKAFLTLTTCRKLLGLAG
SEQIDNO:11	241T.....D
SEQIDNO:32	241D
SEQIDNO:2	301	IDYTSIMNEHLNKEKEEFVRNLP TSLNTFSNPYAKVKGSDEDAKMIVEAKPGHALVGF
SEQIDNO:11	301I.....
SEQIDNO:32	301
SEQIDNO:2	361	EMSND SITVLKVYEAKLKQNYQVDKDSLSEVIYGDTDKLFCDQSEQIYYTNNIVFPNEY
SEQIDNO:11	361I.....M.....I.....
SEQIDNO:32	361
SEQIDNO:2	421	VITKIDFTKKMKTLRYEVTANFYD SSTGEIDLNKKKVESSEAEYRTLSANDDGVYMP LGV
SEQIDNO:11	421
SEQIDNO:32	421
SEQIDNO:2	481	ISFTFLTPINGFGLQADENSRLIT LTCKSYLRELLLATDLSNKETKLIVPPSGFISNIVE
SEQIDNO:11	481
SEQIDNO:32	481
SEQIDNO:2	541	NGSIEEDNLEPWKANNKNAYVDHT GG VNGTKALYVHKDGGFSQFIGDKLKP KTEYVIQYT
SEQIDNO:11	541I.....
SEQIDNO:32	541
SEQIDNO:2	601	VKGKPSIHLK DENTGYIHYEDTNNNLKDYQTITKRFTTGTDLKG VYLILKSQNGDEAWGD
SEQIDNO:11	601E.....N.....
SEQIDNO:32	601
SEQIDNO:2	661	KFTILEIKPAEDLLSPELINPNSWITTPGASISGNKLFINLGTNGTFRQSLSLNSYSTYS
SEQIDNO:11	661
SEQIDNO:32	661
SEQIDNO:2	721	ISFTASGPFNVTVRNSRXVLFERSNLMSSTSHISGTFKTESNNTGLYVELSRRSGGGGHI
SEQIDNO:11	721G.....
SEQIDNO:32	721E.....

SEQIDNO:2	781 SFENVSIK
SEQIDNO:11	781
SEQIDNO:32	781

A “.” means the amino acids are identical at that position.

26 Apr 2007

Alignment Results

EXHIBIT B

Alignment: Global Protein alignment against reference molecule

Parameters: Scoring matrix: BLOSUM 62

Reference molecule: SEQIDNO:2, Region 1-788

Number of sequences to align: 2

Settings: Similarity significance value cutoff: >= 60%

Summary of Percent Matches:

Reference: SEQIDNO:2	1 -	788	(788 aa)	--
Sequence 2: 86BB1(c)	1 -	789	(789 aa)	90%

SEQIDNO:2	1	MNKNNTKLSTRALPSFIDYFNGIYGFIATGIKDIMNMIKFTDTGGNLTLDLILKNQQLLNE
86BB1(c)	1
SEQIDNO:2	61	ISGKLDGVNGSLNDLIAQGNLNTLSKEILKIANEQNQVLNDVNNKLDAINTMLHIYLPK
86BB1(c)	61
SEQIDNO:2	121	ITSMLSDVMKQNYALSLQIEYLSKQLQEISDKLDIINVNVLINSTLTEITPAYQRIKYVN
86BB1(c)	121
SEQIDNO:2	181	EKFEELTFATETTLKVKKDSSPADILDELTELAKSVTKNDVDGFEFYLNTHFDMVVG
86BB1(c)	181G.....S.....Q.....
SEQIDNO:2	241	NNLFGRSALKTASELIAKENVKTSSEVGNVYNFLIVLTALQAKAFLTLTTCRKLLGLAG
86BB1(c)	241D
SEQIDNO:2	301	IDYTSIMNEHLNKEKEEFVRNIPITLSNTFSNPYAKVKGSDAKMIVEAKPGHALVGF
86BB1(c)	301Y.....
SEQIDNO:2	361	EMSNDISITVLKVYEAKLKQNYQVDKDSLSEVIYGDITDKLFCPDQSEIYYTNNIVFPNEY
86BB1(c)	361L.....
SEQIDNO:2	421	VITKIDFTKKMKTLRYEVTANFYDSSTGEIDLNKKKVESSEAEYRTLSANDDGVYMPGLV
86BB1(c)	421
SEQIDNO:2	481	ISSETFLTPINGFGLQADENSRLITLTCKSYLRELLLATDLSNKETKLIVPPSGFISNIVE
86BB1(c)	481G.....L.....
SEQIDNO:2	541	NGSIEEDNLEPWKANNKNAYVDHTGGVNGTKALYVHKDGGFSQFIGDKLKPKEIYVIQYT
86BB1(c)	541
SEQIDNO:2	601	VKGKPSIHLKDENTGYIHYEDTNNNLKDYQTITKRFTTGTDLKGVYLILKSQNGDEAWGD
86BB1(c)	601
SEQIDNO:2	661	KFTILEIKPAEDLLSPELINPNSWITTPGASISGNKLFINLGTNGTFRQSLSLNSYSTYS
86BB1(c)	661	N.T....S.S.K.....T.N.TS.GSTH...T.TLYQ.GR.ILK.N.Q.D.F...R
SEQIDNO:2	721	ISFTASGPFNVTVRNSRXVLFERSNLMSSTSHISGTFKTESNNTGLYVELSRRSG--GGG
86BB1(c)	721	VY.SV..DA..RI....E....K-RY..GAKDV.EM.T.KFEKDNF.T...QGNNLY..P
SEQIDNO:2	779	HISFENVSIK
86BB1(c)	780	IVH.ND....

A "." means the amino acids are identical at that position.